

AMENDMENTS TO THE SPECIFICATION

Please replace the paragraph starting on page 1, line 1, with the following:

This application is a continuation of U.S. Patent Application No. 09/804,690, filed March 12, 2001, which is a continuation of application Ser. No. 09/146,187, filed September 1, 1998, now U.S. Patent No. 6,248,523, which is a division of application Ser. No. 08/977,818, filed Nov. 25, 1997, now U.S. Pat. No. 5,807,995, which is a division of application Ser. No. 08/670,274, filed Jun. 13, 1996, now U.S. Pat. No. 5,891,668, which is a continuation-in-part of application Ser. No. 08/585,758, filed Jan. 16, 1996, U.S. Pat. No. 5,679,523 which claims the benefit of U.S. provisional patent application No. 60/006,856, filed Nov. 16, 1995, the disclosures of which are herein incorporated by reference.

Please replace the paragraph starting on page 6, line 3, with the following:

The full length human cDNA contains an ~~1140~~ 1170 bp open reading frame, encoding a ~~380~~ 390 amino acid protein (GenBank Accession No. U82130). The human and mouse cDNAs are 86% identical at the nucleotide level. The predicted proteins are 94% identical and are distinguished by 20 amino acid mismatches and one gap. A coiled-coil domain (human TSG101 aa 231-302) and a proline-rich domain (human TSG101 aa 130-205, 32% proline) typical of the activation domains of transcription factors are highly conserved between the human and mouse proteins, with only one amino acid mismatch in each of the two domains. The leucine zipper motif in the coiled-coil domain of the human TSG101 protein is identical to the one in the mouse protein.

Please replace the paragraph starting on page 33, line 22, with the following:

A 1494 bp cloned human cDNA insert (which was deposited under the Budapest Treaty at the American Type Culture Collection, Manassas, VA 20110-2209 on June 17, 2003 with Accession No. PTA-5265) was termed full length TSG101 cDNA. Sequence analysis of this cDNA identified a 1140 bp open reading frame predicted to encode a 380 amino acid protein with a molecular mass of 42.841 kDa and a pI of 5.87. The human and mouse cDNAs are 86% identical at the nucleotide level. The predicted proteins are 94% identical and are distinguished by 20 amino acid mismatches and one gap. A coiled-coil domain (human TSG101 aa 231-302) and a proline-rich domain (human TSG101 aa 130-205, 32% proline) typical of the activation domains of transcription factors are highly conserved

between the human and mouse proteins, with only one amino acid mismatch in each of the two domains. The leucine zipper motif in the coiled-coil domain of the human TSG101 protein is identical to the one in the mouse protein. Other conserved features identified in human TSG101 include seven putative protein kinase C phosphorylation sites (aa 11, 38, 86, 89, 215, 225, 357), five potential ~~ease~~ casein kinase II phosphorylation sites (aa 38, 210, 249, 265, 290) and three potential N-glycosylation sites (aa 44,150,297). Analysis of the human TSG101 cDNA and protein sequences by the BLAST program search of NCBI database did not reveal any significant homology with the sequences for any other human genes.

Please replace the nucleic acid sequence of SEQ ID NO:3 with the following:

```

1  gaaggggtgtg  cgattgtgtg  ggacggtctg  gggcagccca  gcagcggctg  accctctgcc
61  tgcgggggaag  ggagtcgcca  ggcggccgtc  atggcgggtg  cggagagcca  gctcaagaaa
121 atgggtgtcca  agtacaaata  cagagacctt  actgtacgtg  aaactgtcaa  tgttattact
181 ctatacaaag  atctcaaacc  tgttttggat  tcatatgttt  ttaacgatgg  cagttccagg
241 gaactaatga  acctcactgg  aacaatccct  gtgccttata  gaggtaatac  atacaatatt
301 ccaatatgcc  tatggctact  ggacacatac  ccatataatc  cccctatctg  ttttgtaaag
361 cctactagtt  caatgactat  taaaacagga  aagcatgttg  atgcaaatgg  gaagatatat
421 ctcccttata  tacatgaatg  gaaacaccca  cagtcagact  tgttggggct  tattcaggtc
481 atgattgtgg  tatttggaag  tgaacctcca  gtcttctctc  gtcctatttc  ggcacacctt
541 ccgccatacc  aggcaacggg  gccaccaaat  acttctctca  tgccaggcat  gccagggtga
601 atctctccat  acccatccgg  ataccctccc  aatcccagtg  gttaccagg  ctgtccttac
661 ccacctgggt  gtccatatcc  tgccacaaca  agttctcagt  acccttctca  gctcctgtg
721 accactgttg  gtcccagtag  ggatggcaca  atcagcgagg  acaccatccg  agcctctctc
781 atctctgcgg  tcagtgaaca  actgagatgg  cggatgaagg  aggaaatgga  tcgtgccag
841 gcagagctca  atgccttgaa  acgaacagaa  gaagacctga  aaaagggtca  ccagaaactg
901 gaagagatgg  ttaccggttt  agatcaagaa  gtagccgagg  ttgataaaaa  catagaactt
961 ttgaaaaaga  aggatgaaga  actcagttct  gctctggaaa  aaatggaaaa  tcagtctgaa
1021 aacaatgata  tcgatgaagt  tatcattccc  acagctccct  tatacaaaaa  gatcctgaat
1081 ctgtatgcag  aagaaaacgc  tattgaagac  actatctttt  acttgggaga  agccttgaga
1141 aggggcgtga  tagacctgga  tgccttcttg  aagcatgtac  gtcttctgtc  ccgtaaacag
1201 ttccagctga  gggcactaat  gcaaaaagca  agaaagactg  ccggtctcag  tgacctctac
1261 tgacttctct  gataccagct  ggaggttgag  ctcttcttaa  agtattcttc  tcttctttt
1321 atcagtaggt  gcccagaata  agttattgca  gtttatcatt  caagtgtaaa  atattttgaa
1381 tcaataatat  attttctgtt  ttcttttggt  aaagactggc  ttttattaat  gcactttcta
1441 tcctctgtaa  actttttgtg  ctgaatgttg  ggactgctaa  ataaaatttg  tttt

```

Please replace the amino acid sequence of SEQ ID NO:4 with the following:

```

MAVSESQLKKMVSKYKYRDLTVRETVNVITLYKDLKPVLD SYVFNDGSSREL MNLTGTIPV P YRGNTYN
IPICLWLLDTPYNPPICFVKPTSSMTIKTGKHVDANGKIYLPYLHEWKHPQSDLLGLIQVMIVVFGDEPPVFSR
PISASYPPYQATGPPNTSYMPGMPGGISPYPSGYPPNPSGYPGCPYPPGGPYPATSSQYPSQPPVTTVGPSRDG
TISED TIRASLISAVSDKLRWRMKEEMDRAQAE LNALKRTEEDLKKGHQKLEEMVTRLDQEVAEVDKNIELLKKK
DEELSSALEKMENQSENNDIDEV I IPTAPLYKQILNLYAEENAIEDTIFYLGEALRRGVIDLDVFLKHVRLLSRK
QFQLRALMQKARKTAGLSDL Y

```